0590
01/31/02

CRF Errors Corrected by the STIC Systems Branch

OIPE

Serial Number: 09/977,283A

ENTERED

CRF Processing Date: 2/12/2002
Edited by:
Verified by: _____ (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where th sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: #3 _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____.
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☑ Other: _Sequence 11 - aligned amino acid nos._ _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

OIPE

RAW SEQUENCE LISTING   DATE: 02/12/2002
PATENT APPLICATION: US/09/977,283A   TIME: 10:55:02

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\02122002\I977283A.raw

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  5 <110> APPLICANT: Reed, Guy L.
  9 <120> TITLE OF INVENTION: Composition and Method for Enhancing Fibrinolysis
 13 <130> FILE REFERENCE: 0609.4320003
 17 <140> CURRENT APPLICATION NUMBER: 09/977,283A
 19 <141> CURRENT FILING DATE: 2001-10-16
 23 <150> PRIOR APPLICATION NUMBER: 08/934,000
 25 <151> PRIOR FILING DATE: 1997-09-19
 29 <150> PRIOR APPLICATION NUMBER: 60/026,356
 31 <151> PRIOR FILING DATE: 1996-09-20
 35 <160> NUMBER OF SEQ ID NOS: 81
 39 <170> SOFTWARE: PatentIn version 3.1
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 60 <221> NAME/KEY: MISC_FEATURE
 62 <222> LOCATION: (1)..(1)
 64 <223> OTHER INFORMATION: May be any Amino Acid
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117 <222> LOCATION: (1)..(1)
119 <223> OTHER INFORMATION: May be any Amino Acid
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RAW SEQUENCE LISTING   DATE: 02/12/2002
PATENT APPLICATION: US/09/977,283A   TIME: 10:55:02

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\02122002\I977283A.raw

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148 <221> NAME/KEY: CDS
150 <222> LOCATION: (1)..(381)
152 <223> OTHER INFORMATION:
156 <220> FEATURE:
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160 <222> LOCATION: (1)..(60)
162 <223> OTHER INFORMATION:
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172 <223> OTHER INFORMATION: May be either Gly or Ala
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178 Met Ser Val Leu Thr Gln Val Leu Xaa Leu Leu Leu Leu Trp Leu Thr
179 -20             -15             -10                 -5
181 ggt gcc aga tgt gac atc cag atg act cag tct cca gcc tcc cta tct    96
182 Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
183             1               5                  10
185 gca tct gtg gga gaa act gtc acc atc aca tgt cga gca agt ggg aat   144
186 Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn
187         15              20                  25
189 att cac aat tat tta gca tgg tat cag cag aaa cag gga aaa tct cct   192
190 Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro
191     30              35                  40
193 cag ctc ctg gtc tat aat gca aaa acc tta gca gat ggt gtg cca tca   240
194 Gln Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser
195  45              50                  55                  60
197 agg ttc agt ggc agt gga tca gga aca caa ttt tct ctc agg atc aac   288
198 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu Arg Ile Asn
199             65                  70                  75
201 agc ctg cag cct gaa gat ttt ggg agt cat tac tgt caa cat ttt tgg   336
202 Ser Leu Gln Pro Glu Asp Phe Gly Ser His Tyr Cys Gln His Phe Trp
203             80                  85                  90
205 acc act ccg tgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa       381
206 Thr Thr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
207             95                  100                 105
211 <210> SEQ ID NO: 5
213 <211> LENGTH: 127
215 <212> TYPE: PRT
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RAW SEQUENCE LISTING   DATE: 02/12/2002
PATENT APPLICATION: US/09/977,283A   TIME: 10:55:02

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\02122002\I977283A.raw

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244 Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
245               1            5                 10
248 Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn
249        15               20               25
252 Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro
253      30               35               40
256 Gln Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser
257 45              50               55                    60
260 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu Arg Ile Asn
261               65               70                    75
264 Ser Leu Gln Pro Glu Asp Phe Gly Ser His Tyr Cys Gln His Phe Trp
265             80               85               90
268 Thr Thr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
269            95               100            105
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276 <212> TYPE: DNA
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292 <222> LOCATION: (1)..(381)
294 <223> OTHER INFORMATION:
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300 <221> NAME/KEY: sig_peptide
302 <222> LOCATION: (1)..(60)
304 <223> OTHER INFORMATION:
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311 -20              -15            -10                    -5
314 ggt gcc aga tgt gac atc cag atg act cag tct cca gcc tcc cta tct      96
315 Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
316               1            5                 10
318 gca tct gtg gga gaa act gtc acc gtc aca tgt cga gca agt ggg aat      144
319 Ala Ser Val Gly Glu Thr Val Thr Val Thr Cys Arg Ala Ser Gly Asn
320        15               20               25
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323 Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro
324     30                  35               40
326 cag ctc ctg gtc tat aat gca aga acc tta gca gat ggt gtg cca tca    240
327 Gln Leu Leu Val Tyr Asn Ala Arg Thr Leu Ala Asp Gly Val Pro Ser
328 45                  50                  55                  60
330 agg ttc agt ggc agt gga tca gga aca caa tat tct ctc aag atc aac    288
331 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn
332             65                  70                  75
334 agc ctg cag cct gaa gat ttt ggg agt tat tac tgt caa cat ttt tgg    336
335 Ser Leu Gln Pro Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp
336             80                  85                  90
338 agt aat ccg tgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa        381
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360 <400> SEQUENCE: 7
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363 -20                 -15                 -10                 -5
366 Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
367             1                   5                   10
370 Ala Ser Val Gly Glu Thr Val Thr Val Thr Cys Arg Ala Ser Gly Asn
371         15                  20                  25
374 Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro
375     30                  35                  40
378 Gln Leu Leu Val Tyr Asn Ala Arg Thr Leu Ala Asp Gly Val Pro Ser
379 45                  50                  55                  60
382 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn
383             65                  70                  75
386 Ser Leu Gln Pro Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp
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415 <222> LOCATION: (1)..(381)
417 <223> OTHER INFORMATION:
421 <220> FEATURE:
423 <221> NAME/KEY: sig_peptide
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434 -20                 -15                 -10                 -5
437 ggt gcc aga tgt gac atc cag atg act cag tct cca gcc tcc cta tct        96
438 Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
439                  1               5                  10
441 gca tct gtg gga gaa act gtc acc atc aca tgt cga gca agt ggg aat       144
442 Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn
443           15                  20                  25
445 att cac aat tat tta gca tgg tat cag cag aaa cag gga aaa tct cct       192
446 Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro
447       30                  35                  40
449 caa ctc ctg gtc tat aat gca aaa acc tta gca gat ggt gtg cca tca       240
450 Gln Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser
451    45                  50                  55                  60
453 agg ttc agt ggc agt gga tca gga aca caa ttt tct ctc aag atc aac       288
454 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn
455                 65                  70                  75
457 agc ctg cag cct gaa gat ttt ggg agt cat tac tgt caa cat ttt tgg       336
458 Ser Leu Gln Pro Glu Asp Phe Gly Ser His Tyr Cys Gln His Phe Trp
459                 80                  85                  90
461 acc act ccg tgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa         381
462 Thr Thr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
463                 95                  100                 105
467 <210> SEQ ID NO: 9
469 <211> LENGTH: 127
471 <212> TYPE: PRT
473 <213> ORGANISM: Artificial Sequence
477 <220> FEATURE:
479 <223> OTHER INFORMATION: Alpha-2 Antiplasmin Antibody
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489 Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
490                  1               5                  10
493 Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn
494           15                  20                  25
497 Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro
498       30                  35                  40
501 Gln Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser
502    45                  50                  55                  60
505 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn
506                 65                  70                  75
509 Ser Leu Gln Pro Glu Asp Phe Gly Ser His Tyr Cys Gln His Phe Trp
510                 80                  85                  90
513 Thr Thr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
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Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY   DATE: 02/12/2002
PATENT APPLICATION: US/09/977,283A   TIME: 10:55:03

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF3\02122002\I977283A.raw**

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L:125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:575 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:744 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:817 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:912 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:917 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:921 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:925 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:929 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
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L:937 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:941 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:945 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
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L:1442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1472 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:2715 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75
L:2723 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75
L:2727 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75
L:2731 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75
L:2784 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76
L:2953 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:77
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L:3261 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79
L:3344 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80
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L:3601 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81
L:3605 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81
L:3609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81
L:3617 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81
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